

Nucleotide sequence of the maize *R*-*S* gene

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The *R* gene family of maize comprises a set of regulatory loci that control the tissue-specific synthesis of anthocyanin pigments in various parts of the maize plant. Genetic and molecular analyses of these genes have led to the proposal that they encode functionally identical proteins whose diverse pattern of tissue-specific expression reflects differences in their respective promoter sequences (1). We have sequenced a cDNA clone for the seed-specific *R-S* gene. The sequence for *R-S* is 95% similar to that for *Lc*, another member of the *R* family. Most of the differences are localized in the 5' untranslated region, consistent with the notion that the genes have distinct regulatory sequences. The amino acid differences in the protein coding regions are minor and, for the most part, appear to conserve the domains proposed to be important for function of the protein as a putative transcriptional activator (1).

The nucleotide sequence was determined on both strands by the Sanger method. AUG codons in the 5' leader are underlined; the third AUG opens a reading frame of 612 amino acids that terminates at the TGA (underlined) at nucleotide position 1982.

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REFERENCE

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